

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:54 ; Search time 41 Seconds
(without alignments)
1869.308 Million cell updates/sec

Title: US-09-809-827-31
Perfect score: 297
Sequence: 1 MGDHAWFLKDFLAGAVAAA.....LRMGAGFVLVLYDEIKKYV 297

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 30

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Listing first 45 summaries

- Database : SPTEMBL_23.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	81	27.3	298	6	O46373	oryctolagus
2	80	26.9	298	11	Q8BV19	mus musculus
3	48	16.2	170	6	Q9X569	scrofa
4	48	16.2	254	11	Q8BKQ5	mus musculus
5	41	13.8	298	13	Q8JH10	brachydanio
6	39	13.1	298	6	Q8SOH5	bos taurus
7	39	13.1	298	13	Q9YIC4	rana rugosa
8	39	13.1	298	13	Q9PRH2	rana rugosa
9	39	13.1	298	13	Q919M9	xenopus lae
10	39	13.1	298	13	Q9PRH1	rana rugosa
11	39	13.1	298	13	Q8AYM3	gallus gall
12	39	13.1	317	13	Q91336	rana sylvat
13	37	12.5	312	5	Q81RA0	drosofila
14	34	11.4	307	5	O62526	drosofila
15	34	11.4	313	5	Q21103	caenorhabdi
16	34	11.4	313	5	P91410	caenorhabdi

17	32	10.8	300	5	O45865	caenorhabdi
18	32	10.8	300	5	Q17407	caenorhabdi
19	31	10.4	315	4	Q9H0C2	homo sapien
20	30	10.1	288	5	O44094	drosofila
21	30	10.1	288	5	O44093	drosofila
22	30	10.1	300	5	Q9NHWS	lucilia cup

ALIGNMENTS

RESULT 1

O46373 ID O46373 PRELIMINARY; PRT; 298 AA.
AC O46373;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Yamaguchi N., Kasai M.;
RT "Identification of a 30kDa calsequestrin-binding protein, which
regulates calcium release from sarcoplasmic reticulum of rabbit
skeletal muscle";
RL J. Biochem. 335:541-547 (1998).
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB009386; BAA23777.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 27.3%; Score 81; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.3e-74;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VAAAVSKTAVATPIERVKLLQVQHASKQISAEKQYKGIIDCVVRIPKEQPLSFWRGNLA 76
DB 17 VAAAVSKTAVATPIERVKLLQVQHASKQISAEKQYKGIIDCVVRIPKEQPLSFWRGNLA 76
QY 77 NVIRYFPTQALNFAFKDKYKQ 97
DB 77 NVIRYFPTQALNFAFKDKYKQ 97

RESULT 2

O46373 ID O46373 PRELIMINARY; PRT; 298 AA.
AC O46373;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Solute carrier family 25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/60; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK078077; BAC37117.1; -. F94C89009836710B CRC64;
SQ SEQUENCE 298 AA; 32904 MW; 794C89009836710B CRC64;
Query Match 26.9%; Score 80; DB 11; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.7e-73; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0;
QY 18 AA AVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77
DB 18 AA AVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77
QY 78 VIRYPTQALNFAFKDKYK 97
DB 78 VIRYPTQALNFAFKDKYK 97
RESULT 3
Q9XS69 PRELIMINARY; PRT; 170 AA.
AC Q9XS69
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocator 1 (Fragment).
GN ANTL.
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99269917; PubMed=10337623;
RA Larsen N.J., Marklund S., Kelly K.A., Malek M., Tuggle C.K., Yerie M.,
RA Rothschild M.F.;
RT "New insights into porcine-human syntenic conservation.";
RL Mamm. Genome 10:488-491(1999).
DR EMBL; AF055633; AAD20940.1; -.
DR InterPro; IPR001993; Mitoch. carrier.
DR InterPro; IPR002067; Mit. carrier.
DR Pfam; PF00153; mito carr. 2.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
FT NON TER 1
FT NON TER 170
SQ SEQUENCE 170 AA; 18769 MW; C389C14D3C464CB9 CRC64;
Query Match 16.2%; Score 48; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 99 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146
DB 38 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 85
RESULT 4
Q8BKQ5 PRELIMINARY; PRT; 254 AA.
AC Q8BKQ5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK051172; BAC34543.1; -. D85A79F58F2E3B96 CRC64;
SQ SEQUENCE 254 AA; 27931 MW; D85A79F58F2E3B96 CRC64;
Query Match 16.2%; Score 48; DB 11; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.7e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 99 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146
DB 99 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146
RESULT 5
Q8JH10 PRELIMINARY; PRT; 298 AA.
AC Q8JH10
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
GN SLC35A5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22035902; PubMed=12006978;
RA Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
RT essential for early vertebrate development.";
RL Nat. Genet. 31:135-140(2002).
DR EMBL; AF506216; AAM34660.1; -.
DR InterPro; IPR001993; Mitoch. carrier.
DR InterPro; IPR002067; Mit. carrier.
DR InterPro; IPR002030; Mit. uncoupling.
DR Pfam; PF00153; mito carr. 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;
Query Match 13.8%; Score 41; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.3e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 56 DCVVRIPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYK 96
DB 56 DCVVRIPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYK 96
RESULT 6
Q8SQH5 PRELIMINARY; PRT; 298 AA.
AC Q8SQH5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RL differences in its isoforms.";
RL Mitochondrion 1:371-379 (2002).
DR EMBL; AB065433; BAB84673.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 13.1%; Score 39; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 7
Q9YIC4 PRELIMINARY; PRT; 298 AA.
AC Q9YIC4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619 (1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008457; BAA36507.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 8
Q9PRH2 PRELIMINARY; PRT; 298 AA.
AC Q9PRH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619 (1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008460; BAA36510.1; -.
DR EMBL; AB008458; BAA36508.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 9
Q9I9M9 PRELIMINARY; PRT; 298 AA.
AC Q9I9M9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford M.J., Khosrowshahian F., Vazmuza S.L., Liversage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBS databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF231347; AAF63471.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
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RESULT 10
Q9PRH1 PRELIMINARY; PRT; 298 AA.
AC Q9PRH1, 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorph sex chromosomes of
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -
DR EMBL; AB008456; BAA36506.1; -
DR EMBL; AB008461; BAA36511.1; -
DR EMBL; AB008462; BAA36512.1; -
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mit carrier.
DR InterPro; IPR002030; Mit uncoupling.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
DR Membrane; Transmembrane; Transport.
KW SEQUENCE 298 AA; 33054 MW; B0E23AD56F48D36 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db |||||
108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 11
Q8AYM3 PRELIMINARY; PRT; 298 AA.
AC Q8AYM3, 2000 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP antiporter.
GN AVANT.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vaudell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db |||||
108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 12
Q91336 PRELIMINARY; PRT; 317 AA.
AC Q91336, 2000 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana sylvatica (Wood frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=45438;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97398141; PubMed=9256066;
RA Cai Q., Greenway S.C., Storey K.B.;
RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
RT in wood frogs under freezing stress."
RL Biochim. Biophys. Acta 1353:69-78(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97398141; PubMed=9256066;
RA Cai Q., Storey K.B.;
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; U44832; AAA97882.2; -
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mit carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
DR Membrane; Transmembrane; Transport.
KW SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 317;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db |||||
108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 13
Q8IRA0 PRELIMINARY; PRT; 312 AA.
AC Q8IRA0, 2000 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG16944-PC.
GN SESB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vaudell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslér C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpén G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mankulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Benson J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Aeburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003484; AAN09267.1; -;
SQ SEQUENCE 312 AA; 34214 MW; 70D5834E74E168DF CRC64;

Query Match 12.5%; Score 37; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.5e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGSGGAGATSLCFVYPLDFARTRLAAD 144
DB 123 QFWRYFAGNLAGSGGAGATSLCFVYPLDFARTRLAAD 159
RESULT 14
O62526 PRELIMINARY; PRT; 307 AA.
ID O62526;
AC O62526;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ANT2 protein.
GN ANT2 OR CG1683.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Efankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslér C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpén G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mankulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RA Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003484; AAF47956.1; -;
DR EMBL; Y10618; CAA71629.1; -;
DR FlyBase; Fgn002511; Ant2.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.

DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 2.
SQ SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061C0C CRC64;

Query Match 11.4%; Score 34; DB 5; Length 307;
Best Local Similarity 100.0%; Pred.No. 6.3e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146
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Db 123 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 156

RESULT 15

Q211103 Q211103 PRELIMINARY; PRT; 313 AA.
AC Q211103;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE K01H12.2 protein.
GN K01H12.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; Z68218; CAA92472.1; -.
DR WormPep; K01H12.2; CE03454.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 313 AA; 34384 MW; D1E455DDB463C984 CRC64;

Query Match 11.4%; Score 34; DB 5; Length 313;
Best Local Similarity 100.0%; Pred.No. 6.4e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146
|||
Db 130 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 163

Search completed: February 12, 2004, 15:57:13
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:54 ; Search time 17 Seconds
(without alignments)
821.584 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 297

Sequence: 1 MGDHAWFLKDFLAGAVAA.....LRGMGAFVLVLYDEIKKVV 297

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 30

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	130	43.8	298	1 ADT1_HUMAN
2	80	26.9	298	1 ADT1_MOUSE
3	80	26.9	298	1 ADT1_RAT
4	76	25.6	297	1 ADT1_BOVIN
5	39	13.1	298	1 ADT2_HUMAN
6	39	13.1	298	1 ADT2_MOUSE
7	39	13.1	298	1 ADT2_RAT
8	39	13.1	298	1 ADT3_BOVIN
9	39	13.1	298	1 ADT3_HUMAN
10	37	12.5	299	1 ADT_DROME

ALIGNMENTS

RESULT 1

ID ADT1_HUMAN STANDARD; PRT; 298 AA.

AC P12235;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).

DE SLC25A4 OR ANT1.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89236396; PubMed=2541251;

RA Cozens A.L., Runswick M.J., Walker J.E.;

RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";

RL J. Mol. Biol. 206:261-280(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=89340499; PubMed=2547778;

RA Li K., Warner C.K., Hodges J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;

RA "A human muscle adenine nucleotide translocator gene has four exons, RT is located on chromosome 4, and is differentially expressed.";

RL J. Biol. Chem. 264:13998-14004(1989).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=88041149; PubMed=2823286;

RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;

RA "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, RT and coevolution with mitochondrial DNA genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]

RP SEQUENCE OF 1-37 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=88124845; PubMed=2829183;

RA Houldsworth J., Attardi G.;

RA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).

RN [6]

RP VARIANTS PEO PRO-114 AND MET-289.

RX MEDLINE=20385067; PubMed=10926341;

RA Kaukonen J., Juselius J.K., Tiranti V., Kyttala A., Zeviani M., Comi G.P., Keranen J., Peltonen L., Suomalainen A.;

RA "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";

RL Science 289:782-785(2000).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT REPEAT 136 136 F -> L (IN REF. 1).
FT CONFLICT 136 136
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match 26.9%; Score 80; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.3e-72;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAVSTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77
DB 18 AAVSTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77

QY 78 VIRYPTQALNFAFKDKYKQ 97
DB 78 VIRYPTQALNFAFKDKYKQ 97

RESULT 3
ADTI_RAT ADTI_RAT STANDARD; PRT; 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinozaki Y., Kamada M., Yanazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochem. Biophys. Acta 1152:192-196(1993).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----

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DR EMBL; X61667; CAA43842.1; -.
DR EMBL; D12770; BAA02237.1; -.
DR PIR; I60173; I60173.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 26.9%; Score 80; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.3e-72;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAVSTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77
DB 18 AAVSTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77

QY 78 VIRYPTQALNFAFKDKYKQ 97
DB 78 VIRYPTQALNFAFKDKYKQ 97

RESULT 4
ADTI_BOVIN ADTI_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

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CC CC MITOCHONDRIAL INNER MEMBRANE.
CC CC -I- SUBUNIT: Homodimer.
CC CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC CC inner membrane.
CC CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
CC CC -----
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CC CC -----
CC CC EMBL; M131783; AAA30363.1; -.
CC CC EMBL; M24102; AAA30768.1; -.
CC CC PIR; A43646; XWBO.
CC CC InterPro; IPR002067; Mit_carrier.
CC CC InterPro; IPR002030; Mit_uncoupling.
CC CC InterPro; IPR001993; Mitoch_carrier.
CC CC Pfam; PF00153; mito_carr; 3.
CC CC PRINTS; PR00926; MITOCARRIER.
CC CC PRINTS; PR00784; MTUNCOUPLING.
CC CC PROSITE; PS00215; MITOCH_CARRIER; 3.
CC CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC CC Multigene family; Methylation.
CC CC INIT_MET 0
CC CC MOD_RES 0 1 BLOCKED.
CC CC MOD_RES 51 51 METHYLATION (POTENTIAL).
CC CC TRANSMEM 11 28 1 (POTENTIAL).
CC CC TRANSMEM 72 90 2 (POTENTIAL).
CC CC TRANSMEM 116 133 3 (POTENTIAL).
CC CC TRANSMEM 175 194 4 (POTENTIAL).
CC CC TRANSMEM 213 230 5 (POTENTIAL).
CC CC TRANSMEM 272 290 6 (POTENTIAL).
CC CC REPEAT 1 110 1.
CC CC REPEAT 111 207 2.
CC CC REPEAT 208 297 3.
CC CC SEQUENCE 297 AA; 32836 MW; A582D3C4A40AE848 CRC64;
CC CC -----
Query Match 25.6%; Score 76; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 7e-68;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 SKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVIRIPKEQGLSFWRGNLANVIRY 81
DB 21 SKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVIRIPKEQGLSFWRGNLANVIRY 80
QY 82 FPTQALNFAFKDKYKQ 97
DB 81 FPTQALNFAFKDKYKQ 96
RESULT 5
ADT2 HUMAN
ID ADT2 HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP-ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
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RT RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT RT cloning and sequence."
RL RL J. Biol. Chem. 265:16060-16063 (1990).
RN RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT RT growth-regulated."
RL RL J. Biol. Chem. 262:4355-4358 (1987).
RN RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
RA Mazzarella R.A., Schlesinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozersky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
CC CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC CC MITOCHONDRIAL INNER MEMBRANE.
CC CC -I- SUBUNIT: Homodimer.
CC CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC CC inner membrane.
CC CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; M57424; AAA51737.1; -.
CC CC EMBL; J02683; AAA35579.1; -.
CC CC EMBL; L78810; AAB39266.1; -.
CC CC EMBL; AC004000; AAB96347.1; -.
CC CC EMBL; J03591; AAA36749.1; -.
CC CC PIR; A29132; A29132.
CC CC Genew; HGNC:10991; SLC25A5.
CC CC MIM; 300150; -.
CC CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC CC GO; GO:0015207; F:adenine transporter activity; TAS.
CC CC GO; GO:0006832; P:small molecule transport; TAS.
CC CC InterPro; IPR002067; Mit_carrier.
CC CC InterPro; IPR002030; Mit_uncoupling.
CC CC InterPro; IPR001993; Mitoch_carrier.
CC CC Pfam; PF00153; mito_carr; 3.
CC CC PRINTS; PR00926; MITOCARRIER.
CC CC PRINTS; PR00784; MTUNCOUPLING.
CC CC PROSITE; PS00215; MITOCH_CARRIER; 3.
CC CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC CC Multigene family.
CC CC TRANSMEM 12 29 1 (POTENTIAL).
CC CC TRANSMEM 73 91 2 (POTENTIAL).
CC CC TRANSMEM 117 134 3 (POTENTIAL).
CC CC TRANSMEM 176 195 4 (POTENTIAL).
CC CC TRANSMEM 214 231 5 (POTENTIAL).
CC CC TRANSMEM 273 291 6 (POTENTIAL).
CC CC REPEAT 1 111 1.
CC CC REPEAT 112 208 2.
CC CC REPEAT 209 298 3.
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FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 G -> E (IN REF. 2).
FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 13.18; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 6
ADT2 MOUSE
ID ADT2_MOUSE STANDARD; PRT; 298 AA.
AC P51881; Q61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudoautosomal genes and their mouse
homologs.";
RL Mamm. Genome 7:25-30(1996).
RN [2]
SQ SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
SQ SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Costet P., Laplace C.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
REVISONS.
RA Laplace C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
SQ SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
translocase 1 and 2 genes.";
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC
DR EMBL; U27316; AAC52838.1; -.
DR EMBL; U10404; AAA19009.1; -.
DR EMBL; X70847; CAAS0196.1; -.
DR EMBL; AF240003; AAF64471.1; -.
DR MGD; MGI:1353496; SLC25a5.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR020303; Mit_uncoupling.
DR Pfam; PF0153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 7
ADT2_RAT
ID ADT2_RAT STANDARD; PRT; 298 AA.
AC Q09073;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
SKELETAL MUSCLE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC EMBL; D12771; BAA02238.1; -
CC InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; Mitoch_carrier.
DR PRINTS; PR00926; MitocARRIER.
DR PROSITE; PS00215; Mitoch_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAAGATSLCFVYPLDPARTRLAADVG 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDPARTRLAADVG 146

RESULT 8
ADT3_BOVIN STANDARD; PRT; 298 AA.
AC P32007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP, ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
CC -|- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -|- SUBUNIT: Homodimer.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -|- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -|- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M24103; AAA30769.1; -
DR PIR; B43646;
DR InterPro; IPR002067; Mit_carrier.

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DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PR00926; MitocARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAAGATSLCFVYPLDPARTRLAADVG 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDPARTRLAADVG 146

RESULT 9
ADT3_HUMAN STANDARD; PRT; 298 AA.
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP, ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89216396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.M., Hong L.,
RA Diachenko L., Marusina K., Sodergren E.J., Lu X., Gibbs R.A.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkeley; TISSUE=Larva, Ovary, and Pupae;
 RC MEDLINE=22426066; PubMed=12537569;
 RX Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A *Drosophila* full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -i- FUNCTION: Catalyzes the exchange of ADP and ATP across the
 CC mitochondrial inner membrane.
 CC -i- SUBUNIT: Homodimer (By similarity).
 CC -i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -i- DOMAIN: Composed of three homologous domains.
 CC -i- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL; S43651; AAB23114.1; -;
 DR EMBL; S71762; AAB31734.3; -;
 DR EMBL; Y10618; CAA71628.1; -;
 DR EMBL; AE003484; AAF47957.1; -;
 DR EMBL; AY060978; AAL28526.1; -;
 DR EMBL; AY070894; AAL48516.1; -;
 DR FlyBase; FBgn0003360; seqB.
 DR GO; GO:0005743; C-mitochondrial inner membrane; IEP.
 DR GO; GO:0006839; P-mitochondrial transport; IMP.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carri; 2.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat: Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 215 232 5 (POTENTIAL).
 FT TRANSMEM 274 292 6 (POTENTIAL).
 FT CONFLICT 18 19 GI -> QV (IN REF. 1 AND 2).
 FT CONFLICT 81 81 I -> Y (IN REF. 1).
 FT CONFLICT 201 201 MISSING (IN REF. 1 AND 2).
 FT CONFLICT 267 267 G -> A (IN REF. 2).
 FT CONFLICT 268 269 TG -> P (IN REF. 1 AND 2).
 FT CONFLICT 270 270 A -> S (IN REF. 1).
 FT CONFLICT 270 270 A -> C (IN REF. 2).
 SQ SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;
 Query Match 12.5%; Score 37; DB 1; Length 299;
 Best Local Similarity 100.0%; Pred. No. 5e-29;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAD 144
 DB 110 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAD 146

Search completed: February 12, 2004, 15:56:19
 Job time : 17 secs

C;Genetics:
A;Gene: ANCL
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 26.9%; Score 80; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAVSVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSPWNGNLAN 77
Db 18 AAVSVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSPWNGNLAN 77

QY 78 VIRYFPTQALNFAFKDKYKQ 97
Db 78 VIRYFPTQALNFAFKDKYKQ 97

RESULT 3
160173
adenine nucleotide translocator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I60173
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
A;Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat
A;Reference number: I60173; MUID:94002161; PMID:8399300
A;Accession: I60173
A;Status: preliminary; translated from GB/EMBL/DBSJ
A;Molecule type: DNA
A;Residues: 1-298 <RES>
A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
C;Genetics:
A;Gene: ant1
A;Introns: 37/3; 200/1; 247/1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 26.9%; Score 80; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAVSVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSPWNGNLAN 77
Db 18 AAVSVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSPWNGNLAN 77

QY 78 VIRYFPTQALNFAFKDKYKQ 97
Db 78 VIRYFPTQALNFAFKDKYKQ 97

RESULT 4
XWBO
ADP,ATP carrier protein T1 - bovine
N;Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A;Reference number: A43646; MUID:19229093; PMID:2540808
A;Accession: A43646
A;Molecule type: mRNA
A;Residues: 1-298 <POW>
A;Cross-references: GB:M24102; NID:g529414; PIDN:AAA30768.1; PID:g529415

R;Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A;Reference number: A24822; MUID:86295775; PMID:3017341
A;Accession: A24822
A;Molecule type: mRNA
A;Residues: 208-298 <RAS>
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
R;Aquila, H.; Miera, D.; Bullitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A;Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
A;Reference number: A03181; MUID:82188267; PMID:7076130
A;Accession: A03181
A;Molecule type: protein
A;Residues: 2-51,'X',53-70,'X',72-109,'X',111-298 <AQU>
A;Note: residue 52 may be methyllysine
R;Babel, W.; Wächter, E.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A;Title: Amino acid sequence determination of the ADP,ATP carrier from beef heart mitochr
A;Reference number: A61343; MUID:82046808; PMID:6271240
A;Accession: A61343
A;Molecule type: protein
A;Residues: 205-298 <BAB>
R;Oettmeier, W.; Masson, K.; Kalinna, S.
Eur. J. Biochem. 227, 730-733, 1995
A;Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/
A;Reference number: S69369; MUID:95172058; PMID:7867632
A;Accession: S69369
A;Molecule type: protein
A;Residues: 49-63;154-168 <OET>
C;Comment: This protein is synthesized in the cytosol and transported into the mitochondr
C;Complex: homodimer
C;Function:
A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP generat
A;Note: located in the inner mitochondrial membrane
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochor
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F;52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 25.6%; Score 76; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.2e-67;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SXTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSPWNGNLANVIRY 81
Db 22 SXTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSPWNGNLANVIRY 81

QY 82 FPTQALNFAFKDKYKQ 97
Db 82 FPTQALNFAFKDKYKQ 97

RESULT 5
A29132
ADP,ATP carrier protein T2 - human
N;Alternate names: mitochondrial ADP,ATP translocase 2
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A29132; C28116
R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulate
A;Reference number: A29132; MUID:87166056; PMID:3031073
A;Accession: A29132
A;Molecule type: mRNA
A;Residues: 1-298 <BAT>
A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: C28116
A;Molecule type: mRNA
A;Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A;Cross-references: GB:J03591; NID:G339720; PIDN:AAA36749.1; PID:G339721
A;Experimental source: clone PHAT3
C;Genetics:

A;Gene: GDB:ANT2; T3; 2F1
A;Cross-references: GDB:125190; OMIM:300150
A;Map position: Xq13-Xq26
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

RESULT 6

S03894
ADP/ATP carrier protein T3 - human
N;Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/ATP
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
A;Accession: S03894; B28116
R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Accession: S03894
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-298 <COZ>
R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116
A;Molecule type: mRNA
A;Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A;Cross-references: GB:J03592; NID:G339722; PIDN:AAA36750.1; PID:G339723
A;Experimental source: liver
C;Genetics:

A;Gene: GDB:ANT3; ANT3Y
A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;2-298/Product: ADP/ATP carrier protein #status predicted <NA>
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

RESULT 7

S31814
ADP/ATP carrier protein T2 - mouse
N;Alternate names: adenine nucleotide translocase
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
A;Accession: S31814
R;Costet, P.; Laplace, C.
submitted to the EMBL Data Library, January 1993
A;Reference number: S31814
A;Accession: S31814
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <COS>
A;Cross-references: EMBL:X70847
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 13.1%; Score 39; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

RESULT 8

B43646
ADP/ATP carrier protein T2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
A;Accession: B43646
R;Powell, S.J.; Mead, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43646
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <POW>
A;Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 13.1%; Score 39; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

RESULT 9

T23207
hypothetical protein K01H12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
A;Accession: T23207
R;McMurray, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19707
A;Accession: T23207
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-313 <EWL>
A;Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

A;Experimental source: clone K01H12

C;Genetics:

A;Gene: CESP:K01H12.2

A;Map position: 4

A;Introns: 4/1; 191/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match

11.4%; Score 34; DB 2; Length 313;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 146

Db 130 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 163

RESULT 10

T25850

hypothetical protein T01B11.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C;Accession: T25850

R;Geisel, C.; Stellyes, L.

submitted to the EMBL Data Library, December 1996

A;Description: The sequence of C. elegans cosmid T01B11.

A;Reference number: Z20099

A;Accession: T25850

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-313 <GEI>

A;Cross-references: EMBL:U80931; PIDN:AA838001.1; GSPDB:GN00022; CESP:T01B11.4

A;Experimental source: strain Bristol N2; clone T01B11

C;Genetics:

A;Gene: CESP:T01B11.4

A;Map position: 4

A;Introns: 4/1; 191/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match

11.4%; Score 34; DB 2; Length 313;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 146

Db 130 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 163

RESULT 11

T25371

hypothetical protein T27E9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C;Accession: T25371

R;Lloyd, C.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20024

A;Accession: T25371

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-300 <WIL>

A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1

A;Experimental source: clone T27E9

C;Genetics:

A;Gene: CESP:T27E9.1

A;Map position: 3

A;Introns: 20/1; 41/3; 115/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match

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Best Local Similarity 100.0%; Pred. No. 1.5e-23;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAAD 144

Db 117 FAGNLASGGAAGATSLCFVYPLDFARTRLAAD 148

Search completed: February 12, 2004, 15:59:06

Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 12, 2004, 15:55:05 ; Search time 33 Seconds
(without alignments)
1884.441 Million cell updates/sec

Title: US-09-809-827-31
Perfect score: 297
Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRMGAGFVLVLYDEIKKTV 297

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 801455 seqs, 209382283 residues

Word size : 30

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	297	100.0	297	9	US-09-811-094-31
2	297	100.0	297	9	US-09-810-644-31
3	297	100.0	297	10	US-09-185-904A-31
4	39	13.1	298	9	US-09-811-094-32
5	39	13.1	298	9	US-09-811-094-33
6	39	13.1	298	9	US-09-810-644-32
7	39	13.1	298	9	US-09-810-644-33
8	39	13.1	298	10	US-09-185-904A-32
9	39	13.1	298	10	US-09-185-904A-33
10	35	11.8	179	12	US-10-029-386-32501
11	34	11.4	87	9	US-09-864-761-36440
12	34	11.4	313	12	US-10-369-493-6072
13	34	11.4	313	12	US-10-369-493-6103
14	32	10.8	300	12	US-10-369-493-5919
15	31	10.4	31	15	US-10-059-261-250

ALIGNMENTS

RESULT 1

US-09-811-094-31
; Sequence 31, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-31

Query Match 100.0%; Score 297; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e-282; Mismatches 0; Indels 0; Gaps 0;
Matches 297; Conservative 0;

QY 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGFSLFWRGNLAVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYFAGNLSG 120
DB 61 IPKEQGFSLFWRGNLAVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDPARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDPARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
QY 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYEPDTRRRMMMQ 240
DB 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYEPDTRRRMMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKRIAKDEGAKAFKGAWSNVLRGMGAGFVLVLYDEIKKTV 297
DB 241 SGRKGADIMYTGTVDCWRKRIAKDEGAKAFKGAWSNVLRGMGAGFVLVLYDEIKKTV 297

RESULT 2

US-09-810-644-31
; Sequence 31, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong

```
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-31

Query Match      100.0%; Score 297; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e-282;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
QY 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
DB 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297

RESULT 3
US-09-185-904A-31
; Sequence 31, Application US/09185904A
; Patent No. US20020171185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-31

Query Match      100.0%; Score 297; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e-282;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
QY 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
DB 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297

RESULT 3
US-09-185-904A-31
; Sequence 31, Application US/09185904A
; Patent No. US20020171185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-31

Query Match      100.0%; Score 297; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e-282;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
QY 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
DB 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
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```
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

Query Match      100.0%; Score 297; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
QY 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
DB 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297

RESULT 4
US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

Query Match      13.1%; Score 39; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146
DB 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146

RESULT 5
US-09-811-094-33
; Sequence 33, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-33

Query Match      13.1%; Score 39; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146
DB 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146
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; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-33

Query Match      13.1%; Score 39; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146
      |||||||
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146

RESULT 6
US-09-810-644-32
; Sequence 32, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32

Query Match      13.1%; Score 39; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146
      |||||||
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146

RESULT 7
US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-33

Query Match      13.1%; Score 39; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146
      |||||||
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146

RESULT 8
US-09-185-904A-32
; Sequence 32, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32

Query Match      13.1%; Score 39; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146
      |||||||
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146

RESULT 9
US-09-185-904A-33
; Sequence 33, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-33
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US-09-185-904A-33

Query Match 13.1%; Score 39; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

Db 108 QWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 10

US-10-029-386-32501
; Sequence 32501, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32501
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004000.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 2.00e-83

US-10-029-386-32501

Query Match 11.8%; Score 35; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 5.3e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 YFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

Db 75 YFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 109

RESULT 11

US-09-864-761-36440
; Sequence 36440, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36440
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78810.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 6.00e-38
; OTHER INFORMATION: EST_HUMAN HIT: AW935235.1, EVALUE 5.00e-37

US-09-864-761-36440

Query Match 11.4%; Score 34; DB 9; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.6e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 FAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

Db 1 FAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 34

RESULT 12

US-10-369-493-6072
; Sequence 6072, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039

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; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6072
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6072

Query Match      11.4%; Score 34; DB 12; Length 313;
Best Local Similarity 100.0%; Pred. No. 8.5e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 146
Db 130 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 163

RESULT 13
US-10-369-493-6103
; Sequence 6103, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6103
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6103

Query Match      11.4%; Score 34; DB 12; Length 313;
Best Local Similarity 100.0%; Pred. No. 8.5e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 146
Db 130 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 163

RESULT 14
US-10-369-493-5919
; Sequence 5919, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5919
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5919
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Query Match      10.8%; Score 32; DB 12; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 FAGNLASGGAAGATSLCFVYPLDPFARTRLAAD 144
Db 117 FAGNLASGGAAGATSLCFVYPLDPFARTRLAAD 148

RESULT 15
US-10-059-261-250
; Sequence 250, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 250
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-261-250
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Query Match      10.4%; Score 31; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DRHKQFWRYFAGNLASGGAAGATSLCFVYPL 134
Db 1 DRHKQFWRYFAGNLASGGAAGATSLCFVYPL 31

Search completed: February 12, 2004, 15:58:33
Job time : 34 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:59 ; Search time 21 Seconds
(without alignments)
598.396 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 297
Sequence: 1 MGDHWSFLKDFLAGAVAA.....LRGMGAFVLVLYDEIKKTV 297

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

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Word size : 30

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	297	100.0	297	4	US-09-434-354-47
2	80	26.9	298	3	US-08-961-871-10
3	39	13.1	298	4	US-09-434-354-48
4	39	13.1	298	4	US-09-434-354-49

ALIGNMENTS

RESULT 1
US-09-434-354-47
; Sequence 47, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-47

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Best Local Similarity 100.0%; Pred. No. 4.9e-278;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAEQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAEQYKGIIDCVVR 60

QY 61 IPKEQGFLSFRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120
DB 61 IPKEQGFLSFRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLSG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180

QY 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVAAGLLSYDPDTRRRMMNQ 240
DB 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVAAGLLSYDPDTRRRMMNQ 240

QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKTV 297
DB 241 SGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKTV 297

RESULT 2
US-08-961-871-10
; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,871
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,017
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 78-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-871-10

Query Match      26.9%; Score 80; DB 3; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.7e-69;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPKQGFSLFWRGNLN 77
Db 18 AAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPKQGFSLFWRGNLN 77
Qy 78 VIRYFPTQALNFAFKDKYKQ 97
Db 78 VIRYFPTQALNFAFKDKYKQ 97

RESULT 3
US-09-434-354-48
; Sequence 48, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-48

Query Match      13.1%; Score 39; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.4e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146

RESULT 4
US-09-434-354-49
; Sequence 49, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 49
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-49

Query Match      13.1%; Score 39; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.4e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADVG 146

Search completed: February 12, 2004, 15:57:46
Job time : 21 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:54 ; Search time 41 Seconds
(without alignments)
1149.800 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 297

Sequence: 1 MGDHAWFLKDFLAGAVAAA.....LRMGAGFLVLYDEIKKYV 297

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 30

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Post-processing: Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	297	100.0	297	21	AAU01199
2	297	100.0	297	22	AAU01200
3	297	100.0	297	23	AAU01378
4	80	26.9	293	22	ABU53219
5	80	26.9	298	19	AAW61169
6	39	13.1	283	22	ABG27056
7	39	13.1	298	21	AAU01032
8	39	13.1	298	21	AAU01033
9	39	13.1	298	22	AAW39641

10	39	13.1	298	22	AAU01199	Human adenine nucl
11	39	13.1	298	22	AAU01200	Human adenine nucl
12	39	13.1	298	23	AAU018516	Human insulin rece
13	39	13.1	298	23	AAU01379	Human adenine nucl
14	39	13.1	298	23	AAU01380	Human adenine nucl
15	39	13.1	323	22	AAU01427	Human polypeptide
16	39	13.1	429	24	ABR41715	Human DITRP organe
17	37	12.5	299	22	ABB66082	Drosophila melanog
18	37	12.5	299	22	ABB67300	Drosophila melanog
19	34	11.4	87	22	ABG50570	Human liver peptid
20	34	11.4	87	22	ABB30549	Peptide #3200 enco
21	34	11.4	87	22	ABB35714	Peptide #3220 enco
22	34	11.4	87	22	ABB21142	Protein #3141 enco
23	34	11.4	87	22	AAU56523	Human brain expres
24	34	11.4	87	22	AAU68905	Human bone marrow
25	34	11.4	87	22	AAU16728	Peptide #3162 enco
26	34	11.4	87	22	AAU29216	Peptide #3253 enco
27	34	11.4	87	22	AAU04445	Peptide #3127 enco
28	34	11.4	87	23	ABG38486	Human peptide enco
29	34	11.4	307	22	ABB58380	Drosophila melanog
30	31	10.4	31	23	ABP56153	PTPC-interacting T
31	31	10.4	31	23	ABP56167	PTPC-interacting S
32	31	10.4	315	22	ABU53218	Human metabolism-a
33	31	10.4	315	23	AAE21175	Human TRICH-19 pro
34	31	10.4	325	22	ABG15423	Novel human diagno
35	30	10.1	136	22	ABG18921	Novel human diagno
36	30	10.1	228	23	ABP43205	Human ovarian anti

ALIGNMENTS

RESULT 1
AAU71031
ID AAY71031 standard; Protein; 297 AA.

AC AAY71031;

DT 29-AUG-2000 (first entry)

XX Human adenine nucleotide translocator ANTL.

XX Human; adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurotropic;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dyaconia;
KW diabetes; Leber's hereditary optic neuropathy; lactic acidosis; stroke; MIDD;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

XX WO200026370-A2.

PD 11-MAY-2000.

XX 03-NOV-1999; 99WO-US25883.

XX 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;

PI Ghosh SS;

XX WPI; 2000-365619/31.

DR N-PSDB; AAD00519.

XX Recombinant construct encoding adenine nucleotide translocator

PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 PS Claim 44; Page 172; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANTL1 from human brain.

XX Sequence 297 AA;
 SQ
 Query Match 100.0%; Score 297; DB 21; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.7e-274;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMQ 240
 DB 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMQ 240
 QY 241 SGRKGADIMYTGTVDCWRKIADKDEGAKAFKPGAWSNVLRGMGAFVLVLYDEIKKYV 297
 DB 241 SGRKGADIMYTGTVDCWRKIADKDEGAKAFKPGAWSNVLRGMGAFVLVLYDEIKKYV 297

RESULT 2
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX
 AC AAU01198;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX
 KW Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX

PR 03-NOV-1999; 99US-0434354.
 XX (MITO-) MITOKOR.
 PA
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri IG;
 PI Velicelcibi G, Davis RE;
 XX
 DR WPI; 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 297; DB 22; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.7e-274; Indels 0; Gaps 0;
 Matches 297; Conservative 0; Mismatches 0;
 QY 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMQ 240
 DB 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMQ 240
 QY 241 SGRKGADIMYTGTVDCWRKIADKDEGAKAFKPGAWSNVLRGMGAFVLVLYDEIKKYV 297
 DB 241 SGRKGADIMYTGTVDCWRKIADKDEGAKAFKPGAWSNVLRGMGAFVLVLYDEIKKYV 297
 RESULT 3
 AAU10378
 ID AAU10378 standard; Protein; 297 AA.
 XX
 AC AAU10378;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 1 (ANT1).

XX Human; adenine nucleotide translocator; ANT;
 KW mitochondrial matrix protein.
 XX Homo sapiens.
 XX WO200185944-A2.
 XX 15-NOV-2001.
 XX 11-MAY-2001; 2001WO-US15416.
 XX 11-MAY-2000; 2000US-0569327.
 XX (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 XX WPI; 2002-055598/07.
 DR N-PSDB; AAS16688.
 XX Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide
 XX Claim 44; Fig 2; 147pp; English.
 XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide.
 CC Preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT1.
 XX SQ Sequence 297 AA;
 Query Match 100.0%; Score 297; DB 23; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.7e-274;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGDHANSFLKDFLAGAANAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 DB 1 MGDHANSFLKDFLAGAANAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKEQGLSPWRGNLANVIRYFPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEQGLSPWRGNLANVIRYFPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREFHGLGDCIIKIPKSDGLRGLYQGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREFHGLGDCIIKIPKSDGLRGLYQGFNVSV 180
 QY 181 QGIIIIYRAAYFGVYDTAKMLPDPKNVHIFVSNWIAQSVTAVAGLLSYPPDTRRRMMQ 240
 DB 181 QGIIIIYRAAYFGVYDTAKMLPDPKNVHIFVSNWIAQSVTAVAGLLSYPPDTRRRMMQ 240
 QY 241 SGRKGADIMYTGTVDCVRKTADEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKYV 297
 DB 241 SGRKGADIMYTGTVDCVRKTADEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKYV 297

RESULT 4
 ABUS3219
 ID ABUS3219 standard; Protein; 293 AA.
 XX AC ABUS3219;
 XX DT 14-APR-2003 (first entry)
 XX DE Human metabolism-associated DKFZphtes3_35n12 homologue #1.
 XX KW Human; gene therapy; vaccine; disease treatment; detection.
 XX OS Homo sapiens.
 XX PN WO200112659-A2.
 XX 22-FEB-2001.
 XX 18-AUG-2000; 2000WO-IB01496.
 XX 18-AUG-1999; 99US-0149499.
 XX 28-SEP-1999; 99US-0156503.
 XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
 XX Wiemann S;
 XX WPI; 2001-327840/34.
 XX Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies -
 XX Example III; Page 850; 1095pp; English.
 XX This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.
 XX SQ Sequence 293 AA;
 Query Match 26.9%; Score 80; DB 22; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-67;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 AAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSPWRGNLAN 77
 DB 14 AAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSPWRGNLAN 73
 QY 78 VIRYPTQALNFAFKDKYKQ 97
 DB 74 VIRYPTQALNFAFKDKYKQ 93
 RESULT 5
 AAW61169
 ID AAW61169 standard; Protein; 298 AA.
 XX AC AAW61169;
 XX DT 28-SEP-1998 (first entry)
 XX DE Ant1 protein.
 XX Ant1; Adenine nucleotide translocator; cloning; screening;
 KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
 KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
XX Mus sp.
XX WO9819714-A1.
XX 14-MAY-1998.
XX 31-OCT-1997; 97WO-US19882.
XX 01-NOV-1996; 96US-0030017.
XX (UYEM-) UNIV EMORY.
XX Graham BC, Macgregor GR, Wallace DC;
XX MPI; 1998-286608/25.
XX N-PSDB; AAV36479.
XX Mice lacking heart-muscle adenine nucleotide translocator protein -
XX useful as model for mitochondrial myopathy and hypertrophic
XX cardiomyopathy in animals and to test therapeutic compositions or
XX gene therapies
XX Disclosure; Page 39-40; 61pp; English.
XX The present sequence is the mouse Ant1 protein, the cDNA producing this
XX polypeptide is cloned by screening a mouse heart cDNA library with the
XX human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by
XX the dideoxy terminator cycle sequencing. The Ant1 protein is encoded by
XX the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
XX in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
XX which can then be converted into ATP. An Ant1 homozygous mutant would
XX thus be defective in OXPHOS which results in disease in oxidative
XX metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
XX used as a model system for fascioscapular humeral muscular dystrophy,
XX hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
XX systems can be used to test possible therapeutic compounds which
XX increase/mediate ATP and ADP exchange across the mitochondrial membrane
XX independent of ANT1.
XX Sequence 298 AA;
Query Match 26.9%; Score 80; DB 19; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.1e-67;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 AAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77
Db 18 AAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77
Qy 78 VIRYFPTQALNFAFKDKYKQ 97
Db 78 VIRYFPTQALNFAFKDKYKQ 97
RESULT 6
ABG27056
ID ABG27056 standard; Protein; 263 AA.
XX
AC ABG27056;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27047.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.

XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX MPI; 2001-639362/73.
XX N-PSDB; AAS91243.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX Claim 20; SEQ ID No 57415; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 263 AA;
Query Match 13.1%; Score 39; DB 22; Length 263;
Best Local Similarity 100.0%; Pred. No. 1e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 108 QFWRYFAGNLASGGAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLASGGAGATSLCFVYPLDFARTRLAADV 146
RESULT 7
AAV71032
ID AAV71032 standard; Protein; 298 AA.
XX
AC AAV71032;
XX
DT 29-AUG-2000 (first entry)
XX
DE Human adenine nucleotide translocator ANT2.
XX
KW Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; nootropic;
KW antiparkinsonian; cytotostatic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;

KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 OS Homo sapiens.
 XX WO200026370-A2.
 XX 11-MAY-2000.
 XX 03-NOV-1999; 99WO-US25883.
 XX 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR WPI; 2000-365619/31.
 DR N-PSDB; AAD00520.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX Claim 45; Page 172-173; 175pp; English.
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX Sequence 298 AA;
 SQ
 Query Match 13.1%; Score 39; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 108 QFWRYFAGNLAGGGAAGATSLCFVYPLDFARTLADVG 146
 DB 108 QFWRYFAGNLAGGGAAGATSLCFVYPLDFARTLADVG 146
 RESULT 8
 AAY71033
 ID AAY71033 standard; Protein; 298 AA.
 XX AAY71033;
 AC AAY71033;
 XX 29-AUG-2000 (first entry)
 DT Human adenine nucleotide translocator ANT3.
 DE Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
 XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotropic;
 KW antifarnesin; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;

KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 OS Homo sapiens.
 XX WO200026370-A2.
 XX 11-MAY-2000.
 XX 03-NOV-1999; 99WO-US25883.
 XX 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR WPI; 2000-365619/31.
 DR N-PSDB; AAD00521.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX Claim 46; Page 173-174; 175pp; English.
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 XX Sequence 298 AA;
 SQ
 Query Match 13.1%; Score 39; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 108 QFWRYFAGNLAGGGAAGATSLCFVYPLDFARTLADVG 146
 DB 108 QFWRYFAGNLAGGGAAGATSLCFVYPLDFARTLADVG 146
 RESULT 9
 AAM39641
 ID AAM39641 standard; Protein; 298 AA.
 XX AAM39641;
 AC AAM39641;
 XX 22-OCT-2001 (first entry)
 DT Human polypeptide SEQ ID NO 2786.
 DE Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 XX Human; peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI58797.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 298 AA;
 Query Match 13.1%; Score 39; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 108 QFWRYFAGNLAGSGAGATSLCFVYPLDFARTLAADVG 146
 DB 108 QFWRYFAGNLAGSGAGATSLCFVYPLDFARTLAADVG 146
 RESULT 10
 AAU01199
 ID AAU01199 standard; Protein; 298 AA.
 XX
 AC AAU01199;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;

KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelcibi G, Davis RE;
 XX
 DR WPI; 2001-291054/30.
 DR N-PSDB; AAS05902.
 XX
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA;
 Query Match 13.1%; Score 39; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 108 QFWRYFAGNLAGSGAGATSLCFVYPLDFARTLAADVG 146
 DB 108 QFWRYFAGNLAGSGAGATSLCFVYPLDFARTLAADVG 146
 RESULT 11
 AAU01200
 ID AAU01200 standard; Protein; 298 AA.
 XX
 AC AAU01200;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;

KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Velicelebi G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB; AAS05903.
 XX
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA;
 Query Match 13.1%; Score 39; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146
 Db |||||
 108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146
 RESULT 12
 AAO18516
 ID AAO18516 standard; Protein; 298 AA.
 XX
 AC AAO18516;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Human insulin receptor signaling modifier SEQ ID NO: 54.
 XX
 KW Human; insulin receptor signaling; insulin receptor signaling modifier;
 KW ISM; diabetes; metabolic syndrome; antidiabetic.
 XX
 OS Homo sapiens.
 XX

PN WO200255664-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 11-JAN-2002; 2002WO-US01048.
 XX
 PR 12-JAN-2001; 2001US-261226P.
 PR 12-JAN-2001; 2001US-261303P.
 PR 12-JAN-2001; 2001US-261304P.
 PR 12-JAN-2001; 2001US-261335P.
 PR 12-JAN-2001; 2001US-261336P.
 PR 12-JAN-2001; 2001US-261361P.
 PR 12-JAN-2001; 2001US-261456P.
 PR 12-JAN-2001; 2001US-261457P.
 PR 12-JAN-2001; 2001US-261458P.
 PR 12-JAN-2001; 2001US-261459P.
 PR 12-JAN-2001; 2001US-261461P.
 PR 12-JAN-2001; 2001US-261518P.
 PR 12-JAN-2001; 2001US-261531P.
 PR 12-JAN-2001; 2001US-261532P.
 PR 12-JAN-2001; 2001US-261589P.
 PR 12-JAN-2001; 2001US-261590P.
 PR 12-JAN-2001; 2001US-261694P.
 PR 12-JAN-2001; 2001US-261695P.
 PR 12-JAN-2001; 2001US-261697P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 XX Seidel-Dugan C, Ferguson KC, Kidd T;
 PI
 XX WPI: 2002-599664/64.
 DR N-PSDB; AAL48635.
 XX
 XX Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent -
 XX
 PS Disclosure; Page 160-161; 232pp; English.
 XX
 CC The present invention relates to a method of identifying a candidate
 CC insulin receptor (INR) signaling modulating agent, involving contacting
 CC an assay system comprising an insulin receptor signaling modifier (ISM)
 CC polypeptide or nucleic acid with a test agent, and detecting a test
 CC agent-biased activity of the assay system. The method is useful for
 CC identifying candidate INR signaling modulating agents. ISM genes may be
 CC used as drug targets for treatment of disorders related to INR signaling
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and
 CC polypeptides are useful for identifying and testing agents that modulate
 CC ISM function and for other applications related to the involvement of ISM
 CC in INR signaling, and for identifying subjects having a predisposition to
 CC such diseases associated with INR signaling. The present sequence is an
 CC ISM protein described in the exemplification of the invention.
 XX
 SQ Sequence 298 AA;
 Query Match 13.1%; Score 39; DB 23; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146
 Db |||||
 108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146
 RESULT 13
 AAU10379
 ID AAU10379 standard; Protein; 298 AA.
 XX
 AC AAU10379;
 XX
 DT 14-FEB-2002 (first entry)
 XX

DE Human adenine nucleotide translocator 2 (ANT2).
 XX
 KW Human; adenine nucleotide translocator; ANT; ss;
 KW mitochondrial matrix protein.

OS Homo sapiens.

PN WO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US15416.

XX 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;

XX WPI: 2002-055598/07.

XX N-PSDB; AAS16689.

XX Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -

XX Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide.
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.

XX SQ Sequence 298 AA;

Query Match 13.1%; Score 39; DB 23; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.1e-28; Mismatches 0; Indels 0; Gaps 0;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

Db 108 QWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

RESULT 14

AAU10380

ID AAU10380 standard; Protein; 298 AA.

XX AAU10380;

XX 14-FEB-2002 (first entry)

XX Human adenine nucleotide translocator 3 (ANT3).

XX Human; adenine nucleotide translocator; ANT;

XX mitochondrial matrix protein.

XX Homo sapiens.

XX

PN WO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US15416.

XX 11-MAY-2000; 2000US-0569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;

XX WPI: 2002-055598/07.

XX N-PSDB; AAS16690.

XX Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -

XX Example 3; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide.
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT3.

XX SQ Sequence 298 AA;

Query Match 13.1%; Score 39; DB 23; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.1e-28; Mismatches 0; Indels 0; Gaps 0;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

Db 108 QWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146

RESULT 15

AAU41427

ID AAM41427 standard; Protein; 323 AA.

XX AAM41427;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6358.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

PD

XX 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI60583.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 2; SEQ ID NO 6358; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 323 AA;
Query Match 13.1%; Score 39; DB 22; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146
DB 133 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 171
Search completed: February 12, 2004, 15:55:50
Job time : 42 secs

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